

SEQUENCE LISTING

<110> Barber, Elizabeth K

<120> Gene Expression Control Element DNA

<130> 896034605001

<150> US 60/237,079

<151> 2000-09-30

<160> 33

<170> PatentIn version 3.1

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<211> 137

<212> DNA

<213> human

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<222> (3) .. (137)

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<221> polyA_site

<222> (130) .. (135)

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0996264.092801

<400> 1
at tat aaa gga aaa aga aaa taa cgc aat gga caa gtg gtg aag ctg 47
Tyr Lys Gly Lys Arg Lys Arg Asn Gly Gln Val Val Lys Leu
1 5 10
tga act cag gtg tgc aca att atc agg aac acc cca aaa cca aag tga 95
Thr Gln Val Cys Thr Ile Ile Arg Asn Thr Pro Lys Pro Lys
15 20 25
ggt aga aat agc atg aga agc cgt gtt tga tgt taa tta att 137
Gly Arg Asn Ser Met Arg Ser Arg Val Cys Leu Ile
30 35 40

<210> 2
<211> 996
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<222> (1)..(996)
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<221> misc_feature
<222> (710)..(996)
<223> Nucleotides 710-996 are homologous to a portion of human dystroph
in DNA in the region of exon 79 except that nucleotides 860-996 a
re inverted in comparison to the orientation of the same sequence
in the dystrophin DNA

<400> 2
gtg gtt tga ttg ata gta aaa aaa atg ttc gtt aat aca agt aga gag 48
Val Val Leu Ile Val Lys Lys Met Phe Val Asn Thr Ser Arg Glu
1 5 10 15
taa gta atc aat caa tca ctc ata gcc aag gtg gaa aag atg tat ccc 96
Val Ile Asn Gln Ser Leu Ile Ala Lys Val Glu Lys Met Tyr Pro

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20	25	30	
atc atg gaa tat tcc tgt tct gat aga aat ctt gtg ctt atc tat gga Ile Met Glu Tyr Ser Cys Ser Asp Arg Asn Leu Val Leu Ile Tyr Gly 35 40 45			144
att ctt ttg ata tat att tac att ggg aac ctg aat gta gct tga cat Ile Leu Leu Ile Tyr Ile Tyr Ile Gly Asn Leu Asn Val Ala His 50 55 60			192
ttt tcc atg taa aca cca gta gcc tga tcc aac att aag ctg ata cta Phe Ser Met Thr Pro Val Ala Ser Asn Ile Lys Leu Ile Leu 65 70 75			240
aca aac aac gtg taa tgg ctt cat taa taa ggc ttt gct tct tcc tgg Thr Asn Asn Val Trp Leu His Gly Phe Ala Ser Ser Trp 80 85			288
aaa ctg gtg aaa aat caa acc ttg ttg tgt aca ccc tcg atg cag ctt Lys Leu Val Lys Asn Gln Thr Leu Leu Cys Thr Pro Ser Met Gln Leu 90 95 100			336
ctg tgt tgt ctt cac cca gaa atg ggg aat gat ttc cca aat ggc aaa Leu Cys Cys Leu His Pro Glu Met Gly Asn Asp Phe Pro Asn Gly Lys 105 110 115 120			384
gaa aca gag tga tgc tat cta tct gca cct ttt gta aag tct gtc ttt Glu Thr Glu Cys Tyr Leu Ser Ala Pro Phe Val Lys Ser Val Phe 125 130 135			432
ctt tct ctt tgt ttt cca gga cac aat gta gga agt ctt ttc cac atg Leu Ser Leu Cys Phe Pro Gly His Asn Val Gly Ser Leu Phe His Met 140 145 150			480
gca gat gat ttg ggc aga gcg atg gag tcc tta gta tca gtc atg aca Ala Asp Asp Leu Gly Arg Ala Met Glu Ser Leu Val Ser Val Met Thr 155 160 165			528
gat gaa gaa gga gca gaa taa atg ttt tac aac tcc tga ttc ccg cat Asp Glu Glu Gly Ala Glu Met Phe Tyr Asn Ser Phe Pro His 170 175 180			576
ggg ttt tat aat att cat aca aca aag agg att aga cag taa gag ttt Gly Phe Tyr Asn Ile His Thr Thr Lys Arg Ile Arg Gln Glu Phe 185 190 195			624
aca aga aat aaa tct ata ttt ttg tga agg gta gtg gta tta tac tgt Thr Arg Asn Lys Ser Ile Phe Leu Arg Val Val Val Leu Tyr Cys 200 205 210			672
aga ttt cag tag ttt cta agt ctg tta ttg ttt tgt taa caa tgg cag Arg Phe Gln Phe Leu Ser Leu Leu Leu Phe Cys Gln Trp Gln 215 220 225			720
gtt tta cac gtc tat gca att gta caa aaa agt tat aag aaa act aca Val Leu His Val Tyr Ala Ile Val Gln Lys Ser Tyr Lys Lys Thr Thr 230 235 240			768

tgt aaa atc ttg ata gct aaa taa ctt gcc att tct tta tat gga acg 816
 Cys Lys Ile Leu Ile Ala Lys Leu Ala Ile Ser Leu Tyr Gly Thr
 245 250 255

cat ttt ggg ttg ttt aaa aat tta taa cag tta taa aga aag aat tat 864
 His Phe Gly Leu Phe Lys Asn Leu Gln Leu Arg Lys Asn Tyr
 260 265 270

aaa gga aaa aga aaa taa cgc aat gga caa gtg gtg aag ctg tga act 912
 Lys Gly Lys Arg Lys Arg Asn Gly Gln Val Val Lys Leu Thr
 275 280

cag gtg tgc aca att atc agg aac acc cca aaa cca aag tga ggt aga 960
 Gln Val Cys Thr Ile Ile Arg Asn Thr Pro Lys Pro Lys Gly Arg
 285 290 295

aat agc atg aga agc cgt gtt tga tgt taa tta att 996
 Asn Ser Met Arg Ser Arg Val Cys Leu Ile
 300 305

<210> 3

<211> 13

<212> PRT

<213> human

<400> 3

Met Tyr Pro Ile Met Glu Tyr Ser Cys Ser Asp Arg Asn
 1 5 10

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<211> 13

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Tyr Ile Tyr Ile Gly Asn Leu Asn Val Ala Asp Thr Met
 1 5 10

<210> 5

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<211> 18
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<400> 5

Asp Asp Leu Gly Arg Ala Met Glu Ser Leu Val Ser Val Met Thr Asp
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Glu Glu

<210> 6
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<400> 6
acttacctgt 10

<210> 7
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<212> DNA
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<400> 7
ttataaagaa agaattataa ag 22

<210> 8
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ccttggctat gagtgattga ttgattactt actctctact tg

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gattgatagt aaaaaaatg

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<210> 10

<211> 21

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caatggcagg ttttacacgt c

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<210> 11

<211> 20

<212> DNA

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<210> 12

<211> 22

<212> DNA

<213> human

<400> 12

ctttttcctt tataattctt tc

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0906264-092601
T09260-4929660

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<210> 14
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<222> (1)..(3)
<223> histone methylation site

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<222> (7)..(9)
<223> histone methylation site

<400> 14
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<400> 15

gttcgttaat acaagtag

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ccagtagcct gatccaac

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<400> 18

ggcttcatta ataag

15

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caggacacaa tgtagga

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<400> 26
gacttagaaa ctactg

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<210> 27

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atagacgtgt aaaacctgc

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18

<210> 29

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<400> 29

ctttttcctt tataattcctt tc

22

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Met Phe Val Asn Thr Thr Lys Val Glu Lys Met Tyr Pro Ile Met Glu
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Tyr Ser Cys Ser Asp Arg Asn Leu Val Leu Ile Tyr Gly Ile Leu Leu
20 25 30

Ile Tyr Ile Tyr Ile Gly Asn Leu Asn Met Lys Lys Glu Gln Asn Lys
35 40 45

Cys Phe Thr Thr Pro Asp Ser Arg Met Val Phe Ile Ile Phe Ile Gln
50 55 60

Gln Arg Gly Leu Asp Ser Lys Ser Leu Gln Glu Ile Asn Leu Tyr Phe
65 70 75 80

Cys Glu Gly Phe Tyr Thr Ser Met Gln Leu Tyr Lys Lys Val Ile Arg
85 90 95

Lys Leu His Lys Ile Thr Gln Trp Thr Arg Thr Pro Gln Asn Gln Ser
100 105 110

Glu Val Glu Ile Ala
115

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<223> Certain membrane-spanning segment

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<222> (93)..(113)

<223> Putative membrane-spanning segment

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<222> (124)..(144)

<223> Certain membrane-spanning segment

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<222> (209)..(229)

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<222> (246)..(266)

<223> Putative membrane-spanning segment

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Ala Lys Val Glu Lys Met Tyr Pro Ile Met Glu Tyr Ser Cys Ser Asp
20 25 30

Arg Asn Leu Val Leu Ile Tyr Gly Ile Leu Leu Ile Tyr Ile Tyr Ile
35 40 45

Gly Asn Leu Asn Val Ala Arg His Phe Ser Met Lys Thr Pro Val Ala
50 55 60

Arg Ser Asn Ile Lys Leu Ile Leu Thr Asn Asn Val Lys Trp Leu His
65 70 75 80

Lys Lys Gly Phe Ala Ser Ser Trp Lys Leu Val Lys Asn Gln Thr Leu
85 90 95

Leu Cys Thr Pro Ser Met Gln Leu Leu Cys Cys Leu His Pro Glu Met
100 105 110

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0996264-092804

Gly Asn Asp Phe Pro Asn Gly Lys Glu Thr Glu Arg Cys Tyr Leu Ser
115 120 125

Ala Pro Phe Val Lys Ser Val Phe Leu Ser Leu Cys Phe Pro Gly His
130 135 140

Asn Val Gly Ser Leu Phe His Met Ala Asp Asp Leu Gly Arg Ala Met
145 150 155 160

Glu Ser Leu Val Ser Val Met Thr Asp Glu Glu Gly Ala Glu Lys Met
165 170 175

Phe Tyr Asn Ser Arg Phe Pro His Gly Phe Tyr Asn Ile His Thr Thr
180 185 190

Lys Arg Ile Arg Gln Lys Glu Phe Thr Arg Asn Lys Ser Ile Phe Leu
195 200 205

Arg Arg Val Val Val Leu Tyr Cys Arg Phe Gln Lys Phe Leu Ser Leu
210 215 220

Leu Leu Phe Cys Lys Gln Trp Gln Val Leu His Val Tyr Ala Ile Val
225 230 235 240

Gln Lys Ser Tyr Lys Lys Thr Thr Cys Lys Ile Leu Ile Ala Lys Lys
245 250 255

Leu Ala Ile Ser Leu Tyr Gly Thr His Phe Gly Leu Phe Lys Asn Leu
260 265 270

Lys Gln Leu Lys Arg Lys Asn Tyr Lys Gly Lys Arg Lys Lys Arg Asn
275 280 285

Gly Gln Val Val Lys Leu Arg Thr Gln Val Cys Thr Ile Ile Arg Asn
290 295 300

Thr Pro Lys Pro Lys Arg Gly Arg Asn Ser Met Arg Ser Arg Val Arg
305 310 315 320

Cys Lys Leu Ile

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<400> 32
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 Phe Pro Ile Gln Cys Ile Val His Gln Arg Ser Ile Gln Glu Phe Ile
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 att att att ttc aac cca agt aaa agc aga gag aaa ata gcc acc tcc 96
 Ile Ile Ile Phe Asn Pro Ser Lys Ser Arg Glu Lys Ile Ala Thr Ser
 20 25 30
 acc ata gcc tca gaa gca agc caa cag cct gaa aca gct ttg aaa tga 144
 Thr Ile Ala Ser Glu Ala Ser Gln Gln Pro Glu Thr Ala Leu Lys
 35 40 45
 aaa gtt ggt gtg gcg gtg atg gtg gca gtg ata atg gtg acc gat ggt 192
 Lys Val Gly Val Ala Val Met Val Ala Val Ile Met Val Thr Asp Gly
 50 55 60
 tgg gtg ctg gtg atg gta gtg gta gtt gtg aag gtg gtg atg 234
 Trp Val Leu Val Met Val Val Val Val Val Lys Val Val Met
 65 70 75

0996364-09301